SEQUENCE LISTING

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<110> Cox III, George Norbert
      Case, Casey Christopher
      Eisenberg, Stephen P.
      Jarvis, Eric Edward
      Spratt, Sharon Kaye
      Sangamo Biosciences, Inc.
<120> Regulation of Endogenous Gene Expression in Cells Using
      Zinc Finger Proteins
<130> 019496-002200US
<140> 09/229,037
<141> 1999-01-12
<160> 40
<170> PatentIn Ver. 2.0
<210> 1
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Xaa Xaa His Xaa Xaa Xaa Xaa His
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25 20

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      with two overlapping D-able subsites
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<221> modified base
<222> (1)..(2)
<223> n = g,a,c or t
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<222> (5)
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<222> (8)
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<223> n = a,c or t; if g, then position 10 cannot be g
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<222> (10)
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                                                                    10
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<222> (1)..(2)
<223> n = g,a,c or t
<220>
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<223> n = g,a,c or t
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                                                                   10
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Thr Gly Glu Lys Pro
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<211> 9
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Leu Arg Gln Lys Asp Gly Glu Arg Pro
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<223> upstream 9-base pair ZFP VEGF1 target site
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<222> (14)..(22)
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  Val Pro Ile Pro Gly Lys Lys Gln His Ile Cys His Ile Gln Gly
tgt ggt aaa gtt tac ggc aca acc tca aat ctg cgt cgt cac ctg cgc
                                                                   97
Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu Arg
                                 25
tgg cac acc ggc gag agg cct ttc atg tgt acc tgg tcc tac tgt ggt
                                                                   145
Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
                             40
         35
                                                                   193
aaa cgc ttc acc cgt tcg tca aac ctg cag cgt cac aag cgt acc cac
Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
                                              60
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acc ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg
Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
cgt agt gac cac ctg tcc cgt cac atc aag acc cac cag aat aag aag
                                                                   289
Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
                                                                   298
ggt gga tcc
Gly Gly Ser
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Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu Arg
                                 25
Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
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Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
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Gly Gly Ser
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       site in VEGF promoter
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   Val Pro Ile Pro Gly Lys Lys Gln His Ile Cys His Ile Gln Gly
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     1
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tgt Cys	ggt Gly	aaa Lys	gtt Val 20	tac Tyr	ggc Gly	cag Gln	tcc Ser	tcc Ser 25	gac Asp	ctg Leu	cag Gln	cgt Arg	cac His 30	ctg Leu	cgc Arg	97
tgg Trp	cac His	acc Thr 35	ggc Gly	gag Glu	agg Arg	cct Pro	ttc Phe 40	atg Met	tgt Cys	acc Thr	tgg Trp	tcc Ser 45	tac Tyr	tgt Cys	ggt Gly	145
aaa Lys	cgc Arg 50	ttc Phe	acc Thr	cgt Arg	tcg Ser	tca Ser 55	aac Asn	cta Leu	cag Gln	agg Arg	cac His 60	aag Lys	cgt Arg	aca Thr	cac His	193
acc Thr 65	ggt Gly	gag Glu	aag Lys	aaa Lys	ttt Phe 70	gct Ala	tgc Cys	ccg Pro	gag Glu	tgt Cys 75	ccg Pro	aag Lys	cgc Arg	ttc Phe	atg Met 80	241
cga Arg	agt Ser	gac Asp	gag Glu	ctg Leu 85	tca Ser	cga Arg	cat His	atc Ile	aag Lys 90	acc Thr	cac His	cag Gln	aac Asn	aag Lys 95	aag Lys	289
	gga Gly															298
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Суѕ	: Gly	/ Lys	Val 20		Gly	Gln	. Ser	Ser 25		Leu	Gln	. Arg	His 30	Leu	Arg	
Trp	His	Thr		Glu	Arg	Pro	Phe 40		. Cys	Thr	Trp	Ser 45	Tyr	Cys	Gly	,
Lys	Arç		e Thr	: Arç	ßer	Ser 55		Lev	Gln	Arg	His 60	Lys	Arg	f Thr	His	
Th:		y Glu	ı Lys	s Lys	Phe 70		Cys	s Pro	Glu	1 Cys 75	Pro	Lys	Arg	Phe	Met 80	
Ar	g Sei	c Asp	o Glu	ı Let 85		Arç	g His	s Ile	e Lys 90	s Thr	His	s Glr	n Asr	1 Lys 95	Lys	
Gl	y Gl	y Se:	c													
<2 <2	<210> 18 <211> 29 <212> DNA <213> Artificial Sequence															
<2 <2	20> 23>	Desc site	ript. 1 r	ion (of A	rtif: on (icia top)	l Se	quen and	ce:V	EGF 1	DNA	targ	et		

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<222> (11)..(19)
<223> VEGF DNA ZFP target site 1
<400> 18
                                                                    29
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      complementary (bottom) strand
                                                                    29
atcgatggcg atcctccccg ctatgcatg
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       site 3 complementary (bottom) strand
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cagcacatat gtcacatcca agg	83
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                                                                   33
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tgt ggt aaa gtt tac ggc cag tcc tcc gac ctg cag cgt cac ctg cgc
Cys Gly Lys Val Tyr Gly Gln Ser Ser Asp Leu Gln Arg His Leu Arg
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                                                                   145
Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
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Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
     50
aca ggt gag aag aaa ttt gct tgc ccg gag tgt ccg aag cgc ttc atg
                                                                   241
Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
                      70
 65
cga agt gac gag ctg tct aga cac atc aaa acc cac cag aac aag aaa
                                                                   289
Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
                  85
gac ggc ggt ggc agc ggc aaa aag aaa cag cac ata tgt cac atc caa
                                                                   337
Asp Gly Gly Gly Ser Gly Lys Lys Gln His Ile Cys His Ile Gln
             100
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cgc Arg	tgg Trp 130	cac His	acc Thr	ggc Gly	gag Glu	agg Arg 135	cct Pro	ttc Phe	atg Met	tgt Cys	acc Thr 140	tgg Trp	tcc Ser	tac Tyr	tgt Cys	433
ggt Gly 145	aaa Lys	cgc Arg	ttc Phe	acc Thr	cgt Arg 150	tcg Ser	tca Ser	aac Asn	ctg Leu	cag Gln 155	cgt Arg	cac His	aag Lys	cgt Arg	acc Thr 160	481
cac His	acc Thr	ggt Gly	gag Glu	aag Lys 165	aaa Lys	ttt Phe	gct Ala	tgc Cys	ccg Pro 170	gag Glu	tgt Cys	ccg Pro	aag Lys	cgc Arg 175	ttc Phe	5 2 9
atg Met	cgt Arg	agt Ser	gac Asp 180	cac His	ctg Leu	tcc Ser	cgt Arg	cac His 185	atc Ile	aag Lys	acc Thr	cac His	cag Gln 190	aat Asn	aag Lys	577
aag Lys																589
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Trp	His	Thr 35	Gly	Glu	Arg	Pro	Phe 40	Met	Cys	Thr	Trp	Ser 45	Tyr	Cys	Gly	
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Arg	Ser	Asp	Glu	Leu 85		Arg	His	Ile	Lys 90		His	Gln	Asn	. Lys 95	Lys	• •
Asp	Gly	Gly	Gly 100		Gly	Lys	Lys	Lys 105		His	Ile	Cys	His 110		Gln	
Gly	Cys	Gly 115		Val	Tyr	Gly	Thr 120		Ser	Asn	Leu	Arg 125		His	Leu	
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Met Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys
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Lys Gly Gly Ser
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gaggagtgga agctgctgga cactgctcag cagatcgtgt acagaaatgt gatgctggag 120
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April Reeves

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE \$

In re application of:

G.N. Cox III et al.

Application No.: 09/229,037

Filed: January 12, 1999

For: REGULATION OF ENDOGENOUS

GENE EXPRESSION IN CELLS USING ZINC FINGER PROTEINS

Examiner: J. Lundgren

Group Art Unit: 1631

REVOCATION OF POWER OF ATTORNEY AND NEW POWER OF ATTORNEY

Assistant Commissioner for Patents Washington, D.C. 20231

Sir:

I, Casey Case, Vice President for Research of the assignee, Sangamo BioSciences, Inc. by virtue of an assignment recorded at Reel 010418 and Frame0960 on April 1, 1999 hereby revoke all powers of attorney heretofore existing in the above-identified application and hereby appoint Sean M. Brennan, Ph.D., Reg. No. 39,917, Dahna S. Pasternak, Reg. No. 41,411, Roberta L. Robins, Reg. No. 33,208 and Gary R. Fabian, Reg. No. 33,875 as our attorneys and agents to prosecute said application, and to transact all business in the Patent and Trademark Office connected therewith.

Please direct all further communications regarding this application to:

Sean Brennan,

Sangamo BioSciences, Inc.

501 Canal Blvd., Suite A100

Richmond, California 94804

Date: February 15, 2001

Çasey Case